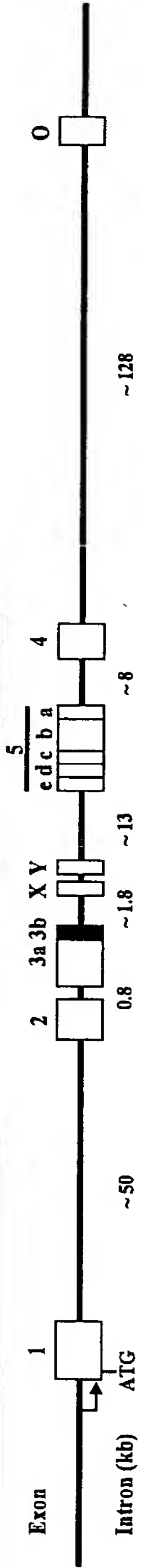


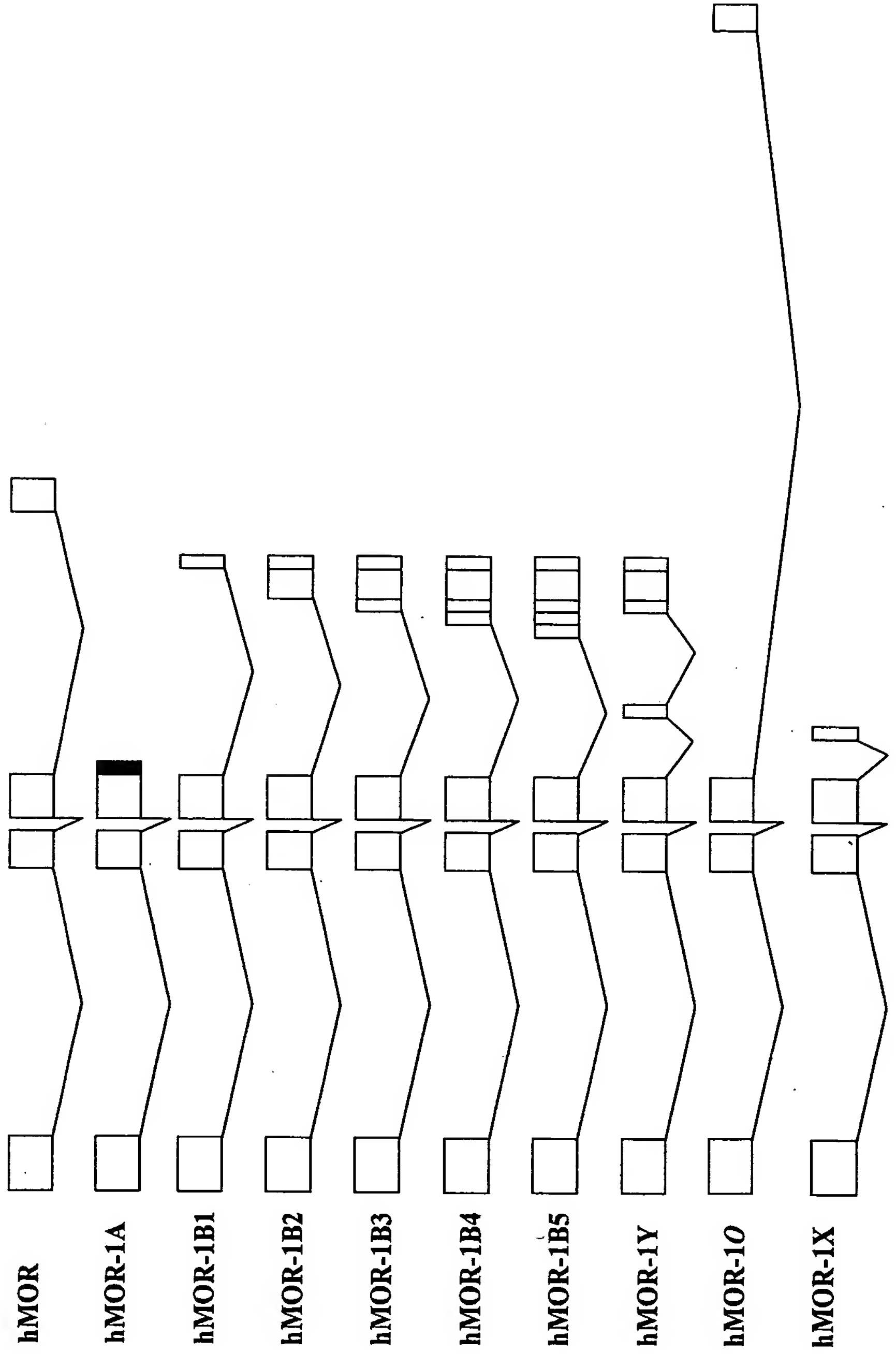
Genomic Structure of the human mu opioid receptor gene

FIG. 1

hBAC clone A (~130 kb)



Alternatively Spliced Variants



hMOR-1A

Exon 3a ↓ Exon 3b
---ACTAATCATCAGGTACGCAGTCTCTAGAAATTAGGTATATCTACTGGGGATGACATAAAATTAAGGCTT
T N H Q V R S L * (SEQ ID NO:27)
TGTGCTAAACTAGGAGTTTAATCCATTATAGAGGATGAGAAATGGAGGGAAGGGAAGCAAGG (SEQ ID NO:28)

hMOR-1B1

Exon 3a ↓ Exon 5a
---ACTAATCATCAGAAATAAGATTATTTCAAAAGTCATCTTTACTCAACTGTGAGCATACCAAGGGCTAATA
T N H Q K I D L F Q K S ^{S#} L L N C E H T K G * (SEQ ID NO:29)
ATTACAATATTTTCCCGTGAAAGAAATATAAGATTGGAAGC (SEQ ID NO:30)

hMOR-1B2

Exon 3a ↓ Exon 5b
---ACTAATCATCAGAGAGAAAGACAGAAATCTGACTGGTAAGAAATTGTTACCCTTTGGCCAGCATGCCA
T N H Q R E R Q K ^{S#} D W * (SEQ ID NO:31)
GGCTTCTGGGTTCCCTTTCCCTGAGCGGCCCTAGTGATCCGGCTTGCGGCACCATCGCCTACGGGCC--- (SEQ ID NO:32)

hMOR-1B3

Exon 3a ↓ Exon 5c
---ACTAATCATCAGGGACCTCCAGCCAAAGTTTGTGCTGACCAACTTGCCGGGTCGTCTTGAAAAGGGGGCTT
T N H Q G P P A K F V A D Q L A G S S * (SEQ ID NO:33)
ACAGGTGTTCCAAGCCCGTGTTTATCCTGAAGTATCCCTCAACACAGAAAAACGACCTCATAACACAAAA--- (SEQ ID NO:34)

hMOR-1B4

Exon 3a ↓ Exon 5d
---ACTAATCATCAGAGCTGACTATGACATGAACCCCTAAATTCCTGTGCC--- (SEQ ID NO:35)
T N H Q S * (SEQ ID NO:36)

FIG. 1B(1)

hMOR-1B5

Exon 3a ↓ **Exon 5e**

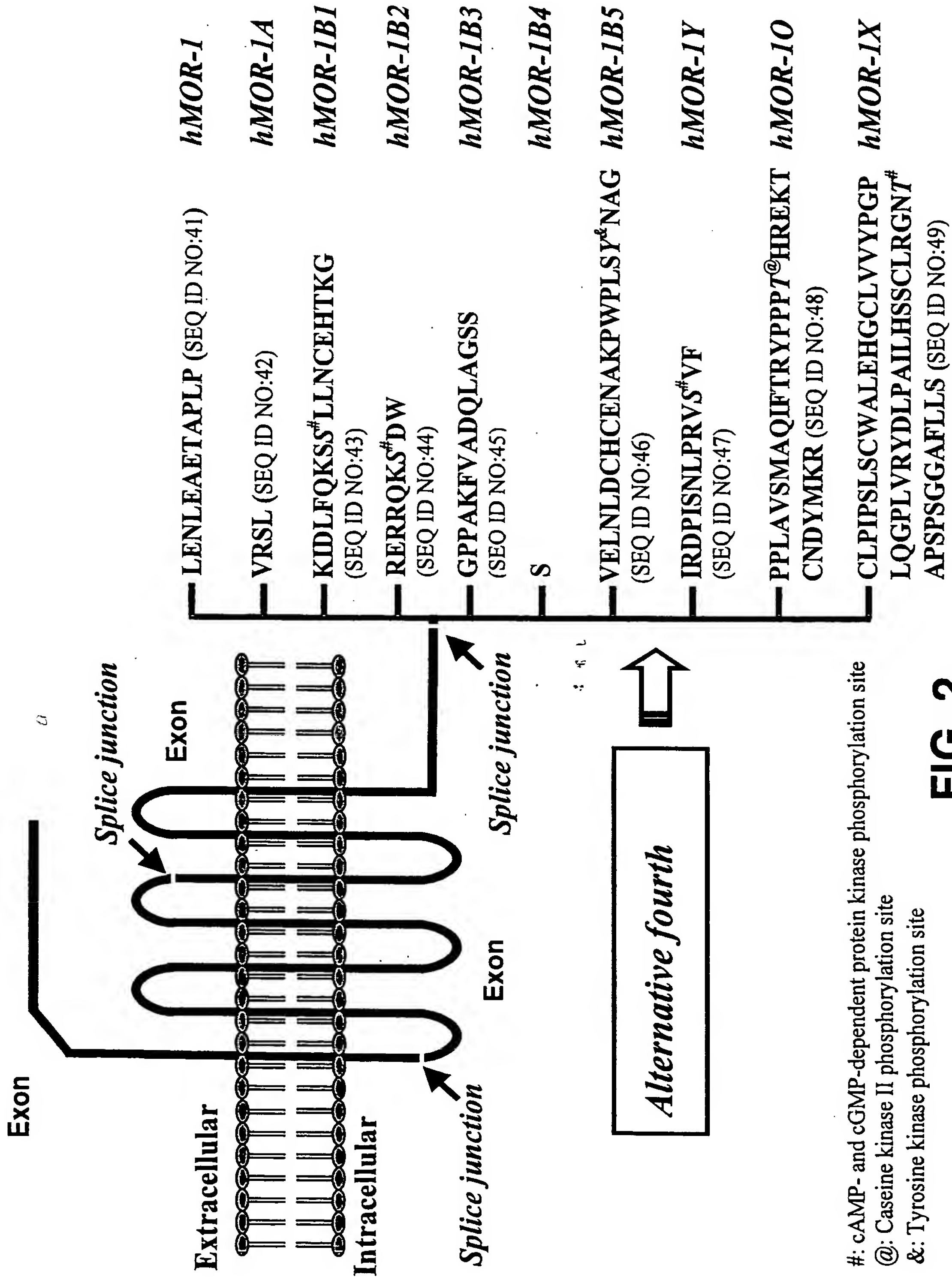
---ACTAATCATCAGGTGGAATTGAACCTGGACTGTCACTGTGAAATGCAAAGCCTTGGCCACTGAGCTACAA
T N H Q V E L N L D C H C E N A K P W P L S Y^e N
TGCAGGGTAGTCTCCATTTCCTTCCCAGGAAGAGTCTAGAGCGTTA--- (SEQ ID NO:37)
A G * (SEQ ID NO:38)

hMOR-1Y

Exon 3a ↓ **Exon Y**

---ACTAATCATCAGATCAGAGATCCAATATCAAACTTCCCAGGGTGTCTGTATTCTGACAACTGTCCACTGA
T N H Q I R D P I S N L P R V S[#] V F * (SEQ ID NO:39)
↓ **Exon 5c**
GGCAATTTCATACAGCGCAAAGTGGAGTGGCGATTGTGGCAGTTATCAAGGGACCTCCAGCCCAAGTT TGTT--- (SEQ ID NO:40)

FIG. 1B(2)



#: cAMP- and cGMP-dependent protein kinase phosphorylation site
 @: Caseine kinase II phosphorylation site
 &: Tyrosine kinase phosphorylation site

FIG. 2

hMOR-1B1 (1354 bp)

CGGAAAGGAGCGGCTGAGGCGCTTGGAACCCGAAAGTCTCGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCGCCC
GGCCGTCAGTACCATGGACAGCAGCGCTGCCCCACGAAACGCCAGCAATTGCACTGATGCCTTGCGCTACTCAAGTTG
CTCCCCAGCACCCAGCCCCGGTTCTGGGTCAACTTGTCCCACTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAAC
CGCACCGACCTGGGCGGAGAGACAGCCTGTGCCCTCCGACCGCAGTCCCTCCATGATCACGGCCATCACGATCATG
GCCCTCTACTCCATCGTGTGCGTGGTGGGCTCTTCGGAAACTTCCTGGTCAATGTGATTGTCAGATACACCAAGAT
GAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGATGCCTTAGCCACCAGTACCCTGCCCTTTTCAGAGT
GTGAATTACCTAATGGGAACATGGCCATTTGGAAACCATCCTTTGCAAGATAGTGATCTCCATAGATTACTATAACATGT
TCACCAGCATATTCACCCCTCTGCACCATGAGTGTGATCGATACATTTGCAGTCTGCCACCCTGTCAAGGCCTTAGATTTC
CGTACTCCCCGAAATGCCAAATATCAATGTCTGCAACTGGATCCTCTCTTCAGCCATTGGTCTTCTGTAAATGTTTCAT
GGCTACAACAAATACAGGCAAGGTTCCATAGATTGTACACTAACATTTCTCTCATCCAAACCTGGTACTGGGAAACCTG
CTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTAATGCCAGTGCTCATCATTAACCGTGTGCTATGGACTGATCTTGGC
CCTCAAGAGTGTCCGCATGCTCTCTGGCTCCAAAGAAAGGACAGGAATCTTCGAAGGATCACCGAGATGGTGTGGT
GGTGGTGGCTGTGTTCATCGTCTGGACTCCCATTCACATTTACGTCAATCAATTAAGCCTTGTTACAAATCCAGAAA
CTACGTTCCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAGGTTACACAAACAGCTGCCCTCAACCCAGTCTTTATGCA
TTTCTGGATGAAAACTTCAAACGATGCTTCAGAGAGTTCTGTATCCCAACCTCTTCCAAACATTGAGCAACAAACTCCA
CTCGAATTCTGTCAGAACACTAGAGACCAACCCCTCCACGGCCAATACAGTGGATAGAACTAATCATCAGAAATAGATT
TATTTCAAAGTCATCTTTACTCAACTGTGAGCATACCAAGGGCTAATAATTACAATATTTTCCCGTGAAAGAATATAA
GATTGGAGC (SEQ ID NO:50)

hMOR-1B1 (406 aa)

MDSSAAPTNASNCTDALAYSSCPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTPIHYYVIKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQKIDLFQKSSLLNCEHTKG (SEQ ID NO:51)

FIG. 3A

hMOR-1B2 (2218 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCGCCGGCGTCAGTACCATGGACAGCGCTGCCCCACGAACG
CCAGCAATTGCACTGATGCCCTTGGCGTACTCAAGTTGCTCCCAAGCACCCAGCCCGGTTCTTGGTCAACTTGTCCCA
CTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAACCGCACCGACCTGGCGGGAGAGACAGCCTGTGCCCCTCCGAC
CGGCAGTCCCTCCATGATCACGGCCATCACGATCATGGCCCTCTACTCCATCGTGTGCGTGGGCTCTTCGGAAAC
TTCCTGGTCATGTATGTGATTCAGATACACCAAGATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGC
AGATGCCCTTAGCCACCAGTACCCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTTGGAAACCATCCTT
TGCAAGATAGTGATCTCCATAGATTACTATAACATGTTCAACCATATTCACCCCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTCTGCCACCCCTGTCAAGGCCCTTAGATTTCCGTACTCCCGAAATGCCAAATTAATCAATGTCTGCAACTG
GATCCTCTCTTCAGCCATTGGTCTTCTCTGTAAATGTTTCATGGCTACAAACAATAACAGGCAAGGTTCCATAGATTGTACAC
TAACATTTCTCTCATCCAAACCTGGTACTGGGAAACACCTGCTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTTATGCCAGTG
CTCATCATTAACCGTGTGCTATGGAATGATCTTGGCCCTCAAGAGTGTCCGCATGCTCTCTGGCTCCAAAGAAAGG
ACAGGAATCTTTCGAAGGATCACCAAGGATGGTGTGGTGTGGTGTGTTTCATCGTCTGTGGACTCCCATTCACAT
TTACGTCAATCAATAAGCCTTGGTTACAATCCAGAAACTACGTTCCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAG
GTTACACAAACAGCTGCCTCAACCCAGTCTTTATGCAATTTCTGGATGAATAACTTCAACGATGCTTCAGAGAGTTCTG
TATCCCAACCTCTTCCAACATTTGAGCAACAATACTCCACTCGAATTCGTCAAGAACACTAGAGACCACCCCTCCACGGCC
AATACAGTGGATAGAACTAATCATCAGAGAGAAAGAACAGAAATCTGACTGGTAAGAAATTGTTACCCCTTTTGCCA
GCATGCCAGGCTTCTGGGTTCCCTTTCCCTGAGCGGCCCTAGTGATCCGGCTTGGCGCACCATCGCCTACGGGCCAAGC⁹
TGCAATCATAAAGGAATTTT²⁶TTTTCATTTCTGGCCAGAGCAAAACACATGTGATAAAACATAGGCATTAGCTACTCTG²⁶
CTTAGCACCAATAATCAGACTAGCTTAAATTTGCCCCAGATGGTTCATCATCTTTAATCCGACCTCTGACTTGCAGT
TTCAACACGTCTCTTTGGGCAAAACAGTTGCCCTGAGTAACAGAAAGATAGGAAAGGAAAGGAGAGAGAGAA
AATGTGCCCAGTGGAAGGTGGGAAGGTGAATGATCAAGAGGCCAGAGAAAGACTCACCTATTGCAGCAACACT
GTAGAAGTTCAGGCAGCTGCTTCTCGGTAGCAAAAGGATCTTTTCCAGCAATCCTATTAGCTCTCAAGTTTCCCCTTTTA
GGGAGGAAAAAGCTCCCCATGTCCCAGATCCTGTACATGTCCAACCCTGCCATCCACAGCCATCAGCAAAAGAGTGCA
AGACAGATTAAATCCAAAGAGAAATAGCAATTAATATCCCATAGCATCAAAAGCTGTTCTTAGCCAAGAGGACTTTAACG
GGAGGGTCTCTAACACCCCTAAATCTTAGAAGAGACTCTAACCATCCTAAGTAGGGCTCTAACCCCGCTTTATAAACT
TTTAAATTGACTCCCATCTTAACAGTTGCAATCCATGGAGGAATGCTTGATAACCTCGGTGATAAGATAAAACCAAGC
ATACTAGAAAGTGTCTCTAAATTAATAAATAACAGTAGTTGCTAGAGAAATAATTTTAGTCCAAATAATCCAACTATAGAA
ACATAGAAATGTGAGAGGTAGCACATAAGAAATAAGTCAATGGGATTTTATTTCATGGACCAGCAATATGATGATAAA
GCCATCTAACC (SEQ ID NO:52)

FIG. 3B(1)

hMOR-1B2 (397 aa)

MDSSAAPNTNASNCTDALAYSSCAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMTAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKATAINIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVVAVFIVCWTPIHYYVIKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQRRERQKSDW
(SEQ ID NO:53)

hMOR-1B3 · (2483 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCGCCGGCTCAGTACCATGGACAGCAGCGCTGCCCCACGAACG
CCAGCAATTGCACCTGATGCCCTTGCGGTACTCAAGTTGCTCCCCAGCACCCAGCCCCGGTTCTCTGGGTCAACTTGTCCCA
CTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAACCGCACCCGACCTGGCGGGAGAGACAGCCTGTGCCCTCCGAC
CGCAGTCCCTCCATGATCACGGCCATCACGATCATGCCCCCTCTACTCCATCGTGTGCGTGGGCTCTTCGGAAAC
TTCCTGGTCATGTA TGTGATTGTCAGATACCAAGATGAAGACTGCCAACACATCTACATTTTCAACCTTGCTCTGGC
AGATGCCCTTAGCCACCAGTACCCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCAATTTGGAACCATCCTT
TGCAAGATAGTATCTCCATAGATTACTATAACATGTTCCACCAGCATATTCAACCCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTCTGCCACCCCTGTCAAGGCCCTTAGATTTCCTACTCCCGAAATGCCAAATTAATCAATGTCTGCAACTG
GATCCTCTCTCAGCCATTGGTCTTCCTGTAAATGTTTCATGGCTACAACAAATACAGGCAAGGTTCCATAGATTGTACAC
TAACATTTCTCTCATCCAACCTGGTACTGGGAAACCTGTCTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTATGCCAGTG
CTCATCATTAACCGTGTGCTATGGA CTGATGATCTTGGCCCTCAAGAGTGTCCGCATGCTCTCTGGCTCCAAAGAAAAGG
ACAGGAATCTTTCGAAGGATCACCAAGGATGGTGTGGTGTGTTTCATCGTCTGTGACTCCCATTCACAT
TTACGTCAATCAATTAAGCCTTGGTTACAATCCCAGAAACTACGTTCCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAG
GTTACACAACAGCTGCCCTCAACCCAGTCTTTATGCAATTTCTGGATGAATACTTCAACGATGCTTCAGAGAGTTCTG
TATCCCAACCTCTTCCAACATTGAGCAACAACCTCCACTCGAATTCGTCAGAACACTAGAGACCACCCCTCCACGGCC
AATACAGTGGATAGAACTAATCATCAGGACCTCCAGCCAAGTTTGTGCTGACCAACTTGCCGGGTCTCTTGAAAAG
GGGCTTACAGGTGTTCCAAGCCCGTGTTTATCCTGAAGTATCCCTCAACACAGAAAACGACCTCATACACAAAAT
ACACCAGCTTAAAAATAGCCTTTTGAAATTAATTTTTCACATTAATCAAACTTTACAGAGGAGATAAACACTGATTTTAT
TTTATTTTATTTTATTTTATTTTATTTGCCATTCAATTCACCGTTTGCACAGAGAGAAAGAACAGATAATCTGACT
GGTAAGAAATTGTTACCCCTTTTGGCCAGCATGCCAGGCTTCTGGGTTCCCTTTCCTGAGCGGCCCTAGTGATCCGGCTTG
CGGCACCATCGCCTACGGGCCAAGCTGCATCATAAAGGAATTTTATTTTTCATTTCTGGCCAGAGCAAAACACATGTGA
TAAACATAGGCATTAGCTACTCTGCTTAGCACCAATATCAGACTAGCTTAAATTTGCCCCCAGACGGGTTCCATCAT
CTTTAATCCGACCTCTGACTTGCA GTTTCAACACGTGCTCTCTGGCAAAACAGTTGCCCTGAGTAACAGAAAAGATAG
GAAAGGAAAAGGAGAGAGAAACGTGCCAGTGGAAAGGTGGGAAGGTGAATGATCAAGGAGGCCAGAGAAA
GACTCACCTATTGCAGCAACACTGTAGAA GTTCAGGCAGCTGCTTCTCGGTAGCAAAAGGATCTTTTCCAGCAATCCTA
TTAGCTCTCAAGTTTCCCTTTTAGGGAGGAAAAGCTCCCCATGTCCCGGATCCTGTACATGTCCAACCTGCCGTCC
ACAGCCATCAGCAAGAGTGCAAGACAGATTAAATCCAAAGAGAAATAGCGATTAAATATCCCATAGCATCAAGCTGTTC
TTAGCCAAGAGGGACTTTAACGAGAGGGTCTCTAACACCTAAATCTTAGAAGAGACTCTAACCATCCTAAGTAGGG
CCTCTAACCCCGCTTTATAA ACTTTTAATTGACTCCCATCTTAACAGTTGCAATCCATGGAGGAATGCTTGATAACCTCG
GTGATAAGATAAAAACCAAGCATACTAGAA GTGTTCTCTAAAAATTAACAGTAGTTGCTAGAGAAAAATTTTA

FIG. 3C(1)

GTCCAAAATCCAACTATAGAAACATAGAAATGTGAGAGGCAGCACAATAAGTCATGGGGATTTTATTTCAT
GGACCAGCAATATGATGATAAAGCCATCTAACC (SEQ ID NO:54)

hMOR-1B3 (403 aa)

MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNL.SHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMTAITIMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVAVFIVCWTPIHYYVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIPTSSNIEQQNSTRIQNTRDHPSTANTVDRJNHQGPPAKFVADQLAGSS (SEQ ID NO:55)

hMOR-1B4 (1251 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCGCCGCGTACCATGGACAGCAGCGCTGCCCCACGAACG
CCAGCAATTGCACTGATGCCTTGCGTACTCAAGTTGCTCCCGAGCACCCGCGTTCTGGGTCAACTTGTCCCA
CTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAAACCGACCGACCTGGCGGGAGAGACAGCCTGTGCCCTCCGAC
CGGCAGTCCCTCCATGATCACGGCCATCACGATCATGGCCCTCTACTCCATCGTGTGCGTGGGCTCTTCGGAAC
TTCCTGGTCATGTATGTGATTGTGATACACCAAGATGAAGACTGCCACCAACATCTACGTTTTCAACCTTGCTCTGGC
AGATGCCCTTAGCCACCAAGTACCCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTGGAACCATCCTT
TGCAAGATAGTGATCTCCATAGATTACTATAACATGTTCAACCGCATATTCACCCCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTCTGCCACCCCTGTCAAGGCCTTAGATTCCGTACTCCCCGAAATGCCAAATTAATCAATGTCTGCAACTG
GATCCTCTCTCAGCCATTGGTCTTCCCTGTAATGTTTCATGGCTACAACAAATACAGGCAAGTTCCATAGATTGTACAC
TAACATTCTCTCATCCAACCTGGTACTGGGAAACCTGCTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTTATGCCAGTG
CTCATCATACCGTGTGCTATGGACTGATGATCTTGGCCCTCAAGAGTGTCCGCATGCTCTCTGGCTCCAAAGAAAGG
ACAGGAATCTTCGAAGGATCACCAAGGATGGTGTGGTGTGTTTCATCGTCTGTGGACTCCCATTCACAT
TTACGTCAATCAATAAGCCTTGGTTACAATCCCAGAACTACGTTCCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAG
GTTACACAACAGCTGCCTCAACCCAGTCTTTATGCATTTCTGGATGAATAACTTCAACGATGCTTCAGAGAGTTCTG
TATCCCAACCTCTTCCACATTTGAGCAACAACAACTCCACTCGAATTCGTGAGAACACTAGAGACCCCTCCACGGCC
AATACAGTGGATAGAACTAATCATCAGAGCTGACTATGACATGAACCCCTAAATTCCTGTTCCTCC (SEQ ID NO:56)

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hMOR-1B4 (389 aa)

MDSSAAPTNASNCTDALAYSSCPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYVFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCMTMSVD
RYIAVCHPVKALDFRTPRNAKIINVNCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIIT
VCYGLMILRLKSVRMLSGSKEKDRNLRIRTRMVLVVAVFIVCWTPIHIVVIKALVTIPETTFQTVSWHFCIALGYTNSCLNP
VLYAFLDENFKRCFREFCIPTSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQ (SEQ ID NO:57)

FIG. 3D

hMOR-1B5 (1402 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCGCCGGCCGTCACTACCATGGACAGCAGCGCTGCCCCACGAACG
CCAGCAATTGCACTGATGCCCTTGGCGTACTCAAGTTGCTCCCCAGCACCCAGCCCGGTTCTCTGGGTCAACTTGTCCCA
CTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAACCGCACCCGACCTGGCGGGAGAGACAGCCTGTGCCCTCCGAC
CGGCAGTCCCTCCATGATCACGGCCATCACGATCATGGCCCTCTACTCCATCGTGTGCGTGGGCTCTTCGGAAAC
TTCCTGGTCATGTATGTGATTGTGATACACCAAGATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGC
AGATGCCCTTAGCCACCAAGTACCCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTGGAAACCATCCTT
TGCAAGATAGTATCTCCATAGATTACTATAACATGTTCAACCAAGCATATTCAACCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTCTGCCACCCCTGTCAAGGCCCTTAGATTTCCTGTAATCCCGTAATGCCAAATTAATCAATGTCTGCAACTG
GATCCTCTCTTCAGCCATTGGTCTTCTCTGTAATGTTTCATGGCTACAACAAATACAGGCAAGTTCCATAGATTGTACAC
TAACATTTCTCTCATCCAAACCTGGTACTGGGAAACCTGCTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTATGCCAGTG
CTCATCATTAACCGTGTGCTATGGACTGATGATCTTTGGCCCTCAAGAGTGTCCGCAATGCTCTCTGGCTCCAAAGAAAGG
ACAGGAATCTTCGAAGGATCACCAAGGATGGTGTGGTGGTGTGTTTCATCGTCTGTGACTCCCATTCACAT
TTACGTCAATCAATTAAGCCTTGGTTACAAATCCAGAAACTACGTTCCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAG
GTTACACAACAGCTGCCCTCAACCCAGTCTTTATGCAATTTCTGGATGAATAACTTCAACGATGCTTCAGAGAGTTCTG
TATCCCAACCTCTTCCACATTTGAGCAACAATACTCCACTCGAATTCTGTCAAGAACTAGAGACCAACCCCTCCACGGCC
AATACAGTGGATAGAACTAATCATCAGGTGGAATTGAACCTGGACTGTCACTGTGAATAATGCAAAAGCCTTGGCCACTG
AGCTACAAATGCAGGGTAGTCTCCATTTCCCTTCCAGGAAGAGTCTAGAGCGTTAAATTTTGAAGTTTGGCAAGGCTTGTA
ACTATTTTCATATGATTTTATAGAGCTGACTATGACATGAACCTTAAATTCCTGTTCCTCC (SEQ ID NO:58)

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hMOR-1B5 (410 aa)

MDSSAAPTNASNCTDALAYSSCPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMITAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRIRTRMVLVVVAVFIVCWTPIHIVIIKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCFREFCIPITSSNIEQQNSTRIQRQNTDRDHPSTANTVDRTNHQVELNLDCHCENAKPWPLSYNAG (SEQ ID
NO:59)

FIG. 3E

hMOR-1Y (2601 bp)

CGGTGCTCCTGGCTACCTCGCACAGCGGTGCCCGCCGGCCGTACCATGGACAGCAGCGCTGCCCCACGAACG
CCAGCAATTGCACTGATGCCCTTGGCGTACTCAAGTTGCTCCCCAGCACCCAGCCCGGTTCTTGGTCAACTTGTCCCA
CTTAGATGGCAACCTGTCCGACCCATGCGGTCCGAACCGCACCGACCTGGCGGGAGAGACAGCCTGTGCCCTCCGAC
CGGCAGTCCCTCCATGATCACGGCCATCACGATCATGGCCCTCTACTCCATCGTGTGCGTGGGCTCTTCGGAAAC
TTCCCTGGTCATGTATGTGATGTGATGATACACCAAGATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGC
AGATGCCCTTAGCCACCAGTACCCTGCCCTTCCAGAGTGTGAATTACCTAATGGGAACATGGCCATTTGGAAACCATCCTT
TGCAAGATAGTGATCTCCATAGATTACTATAACATGTTCAACCATGATATTCACCCCTCTGCACCATGAGTGTGATCGAT
ACATTGCAGTCTGCCACCCCTGTCAAGGCCTTAGATTTCCTGTAATGCTACCCCGAAATGCCAAATTAATCAATGTCTGCAACTG
GATCCTCTCTCAGCCATTGGTCTTCCCTGTAATGTTTCATGGCTACAACAATAACAGGCAAGGTTCCATAGATTGTACAC
TAACATTTCTCTCATCCAACCTGGTACTGGGAAAACCTGCTGAAGATCTGTGTTTTCATCTTCGCCCTTCATTTATGCCAGTG
CTCATCATTAACCGTGTGCTATGGAATGATGATCTTGGCCCTCAAGAGTGTCCGCATGCTCTCTGGCTCCAAGAAAAGG
ACAGGAATCTTCGAAGGATCACCAAGGATGGTGTGCTGGTGTGTTTCATCGTCTGTGGACTCCCATTCACAT
TTACGTCAATCAATAAGCCTTGGTTACAATCCAGAAACTACGTTCCAGACTGTTTCTTGGCACTTCTGCAATTGCTCTAG
GTTACACAACAGCTGCCCTCAACCCAGTCCCTTATGCAATTTCTGGATGAAAACCTTCAACGATGCTTCAAGAGATTCTG
TATCCCAACCTCTTCCAAACATTTAGCAACAAAACCTCCACTCGAATTCGTGAGAACACTAGAGACCACCCCTCCACGGCC¹²
AATACAGTGGATAGAACTAATCATCAGATCAGAGATCCAATATCAACCTTCCCAGGGTGTCTGTATTCTGACAAC¹²
CCTGAGGCAATTTCCATACAGCGCAAAGTGGAGTGGCGATTGCGCAGTTATCAAGGGACCTCCAGCCAAGTTTGTG
CTGACCAACTTGCCGGTCTGTTGAAAAGGGGCTTACAGGTGTTCCAAAGCCCGTGTTTATCCTGAAGTATCCCTCA
ACACAGAAACCGACCTCATACACAAATAACACAGCTTAAATAAGCCTTTGAATTTTTCACATTAATCAAAAC
TTTACAGAGGAGATAAACACTGATTTTATTTTATTTTATTTTATTTTATTTTATTTGCCATTCAATCAACCGTTTG
CACAGAGAAAGAACAGACAGAAATCTGACTGGTAAGAAATTGTTACCCCTTTTGCCAGCATGCCAGGCTTCTGGGTTCC
CTTTCCTGAGCGGCCCTAGTGATCCGGCTTGCGGCACCATCGCCTACGGGCCAAGCTGCATCATAAAGGAAATTTTT
TTTTTTCATTTCTGGCCAGACAAACACATGTGATAAAACATAGGCATTAGCTACTCTGCTTAGCACCAATAATCAGAC
TAGCTTAAATTTGCCCCAGATGGTTCCATCATCTTTAATCCGACCTCTGACTTGCAGTTTTCACCACTGCTCTCTGG
CAAAACAGTTGCCCTGAGTAACAGAAAGATAAGAAAGGAAAGGAGAGAGAAACGTGCCAGTGGAGGGGT
GGGAAGGTGAATGATCAAGGAGGCCAGAGAAAGACTCACCTATTGCAAGCAACACTGTAGAGTTCAGGCACTGC
TTCTCGGTAGCAAAAGGATCTTTTCCGGCAATCCTATTAGCTCTCAAGTTTCCCTTTTAGGGAGGAAAAGCTCCCCAT
GTCCCGGATCCTGTACATGTCCAACCTGCCATCCAGCCATCAGCAAAAGAGTGCAAGACAGATTAAATCCAAGAG
AATAGCAATTAATATCCCATAGCATCAAAAGCTGTTCTTAGCCAAGAGGACTTTAACGAGAGGGGTCTCTAACACCCCTA
AATCTTAGAGAGACCCCTAACCATCTCTAAGTAGGGCCTCTAACCCCGCTTATAAACTTTTAATTGACTCCCATCTAAC

FIG. 3F(1)

AGTTGCAATCCATGGAGGAATGCTTGATAACCTCGGTGATAAGATAAAAAACCAAGCATACTAGAAGTGTCTCTAAA
ATTAAAAATACAGTAGTTGCTAGAGAAAAATTTTAGTCCAAAAATCCAACCTATAGAAACATAGAATGTGAGAGGTAGC
ACATAAGAAATAAGTCATGGGGATTTTATTTCATGGACCAGCAATATGATGATAAAAGCCATCTAACCAAGGGC
(SEQ ID NO:60)

hMOR-1Y (402 aa)

MDSSAAPTNASNCTDALAYSSCPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCPPTGSPSMTAITMALYSIVCVV
GLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDR
YIAVCHPVKALDFRTPRNAKINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRRIITRMVLVVAVFIVCWTPIHYYVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPV
LYAFLDENFKRCREFCIP TSSNIEQQNSTRIRQNTRDHPSTANTVDRTNHQIRDPISNLPVSVF (SEQ ID NO:61)

hMOR-1 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1A (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B1 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B2 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B3 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B4 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1B5 (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1O (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1X (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
hMOR-1Y (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP
Consensus (1) MDSSAAPTNASNCTDALAYSSCSPAPSPGSWVNLSHLDGNLSDPCGPNRTDLGGRDSLCP

61

120

hMOR-1 (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1A (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B1 (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B2 (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B3 (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1B4 (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYVFNALADALAT
hMOR-1B5 (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1O (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1X (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
hMOR-1Y (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT
Consensus (61) PTGSPSMITAITIMALYSIVCWGLFGNFLVMYVIVRYTKMKTATNIYIFNLALADALAT

FIG. 4(1)

121 180
hMOR-1 (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1A (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B1 (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B2 (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B3 (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B4 (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1B5 (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-10 (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1X (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
hMOR-1Y (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF
Consensus (121) STLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPVKALDF

181 240
hMOR-1 (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1A (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B1 (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B2 (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B3 (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B4 (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1B5 (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-10 (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1X (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
hMOR-1Y (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI
Consensus (181) RTPRNAKIINVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFI

FIG. 4(2)

241

300

hMOR-1

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

hMOR-1A

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

hMOR-1B1

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

hMOR-1B2

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

hMOR-1B3

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

hMOR-1B4

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

hMOR-1B5

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

hMOR-10

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

hMOR-1X

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

hMOR-1Y

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

Consensus

(241)

FAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTP

301

360

hMOR-1

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

hMOR-1A

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

hMOR-1B1

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

hMOR-1B2

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

hMOR-1B3

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

hMOR-1B4

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

hMOR-1B5

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

hMOR-10

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

hMOR-1X

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

hMOR-1Y

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

Consensus

(301)

YVIAKALVTIPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPTSSNI

FIG. 4(3)

361 420
hMOR-1 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQLENLEAETAPLP-----
hMOR-1A (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQVRS�-----
hMOR-1B1 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQKIDLFQKSSLLNCEHTKG-----
hMOR-1B2 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQRERRQKSDW-----
hMOR-1B3 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQGPPAKFVADQLAGSS-----
hMOR-1B4 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQS-----
hMOR-1B5 (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQVELNLDCHCENAKPWPLSYNAG-----
hMOR-1O (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQPPLAVSMAQIFTRYPPPTHREKTCNDYMKR--
hMOR-1X (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQCLPIPSLSCWALEHGCLVYPGPLQGPLVRYD
hMOR-1Y (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQIRDPISNLPRVSF-----
Consensus (361) EQQNSTRIRQNTRDHPSTANTVDRTNHQ

421 446
hMOR-1 (401) ----- (SEQ ID NO:62)
hMOR-1A (393) ----- (SEQ ID NO:63)
hMOR-1B1 (407) ----- (SEQ ID NO:51)
hMOR-1B2 (398) ----- (SEQ ID NO:53)
hMOR-1B3 (404) ----- (SEQ ID NO:55)
hMOR-1B4 (390) ----- (SEQ ID NO:57)
hMOR-1B5 (411) ----- (SEQ ID NO:59)
hMOR-1O (419) ----- (SEQ ID NO:64)
hMOR-1X (421) LPAILHSSCLRGNTAPSPSGGAFLLS (SEQ ID NO:65)
hMOR-1Y (403) ----- (SEQ ID NO:61)
Consensus (388) ----- (SEQ ID NO:66)

FIG. 4(4)

rMOR-1A

Exon 3a ↓ Exon 3b
-----AACCCAGGTATGTGCTTTCTAGAATTACGGATAACATATAAAAATACCATATCTGGTA
N H Q V C A F * (SEQ ID NO:67)
CCAGTCTAAGATTAAATCTTTAAGAAGGTCAGTAACTTGAGGCAAGTCC (SEQ ID NO:68)

rMOR-1C1

Exon 3a ↓ Exon 7
-----AACCCAGCCAGCCCTGGCAGTCAGCGTGGCCAGATCTTTACAGGATATCCTTCTCCG
N H Q P A L A V S V A Q I F T G Y P S P
↓ Exon 8
ACTCATGGTGAAAACCCCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGTGGAAGAACGTGGT
T^D H G E K P C K S^D Y R D R P R P C G R T W
CTTTGAAATCGCGTGCAGAAATCCAATGTGGAGCACTTCCATTGTGGAGCCGCATTAACTCTATAA
S⁺ L K S^D R A E S^D N V E H F H C G A A L I Y N
↓ Exon 9a
CAATGTGAATTTCATCTAAACACAGGGATGTGCTAGTGAGAAAGTTTGGAGGTGCAGGC (SEQ ID NO:69)
N V N F I * (SEQ ID NO:70)

FIG. 5(1)

rMOR-1C2

Exon 3a ↓ Exon 7
-----AACCCAGCCAGCCCTGGCAGTCAGCGTGGCCCGAGATCTTTACAGGATATCCTTCTCCG
N H Q P A L A V S V A Q I F T G Y P S P
↓ Exon 8
ACTCATGGTGAAAAACCCCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGTGGAAGAACGTGGT
T^D H G E K P C K S^D Y R D R P R P C G R T W
CTTTGAAATCGCGTGCAGAAATCCAATGTGGAGCACTTCCATTGTGGAGCCGCATTAATCTATAA
S⁺ L K S^D R A E S^D N V E H F H C G A A L I Y N
↓ Exon 9b
CAATGAACATAAATAGGCCAGTGTCTGCTCCAGATGCCCTGCGCACGTGCTCGTGGCCCC
N E L K I G P V S W L Q M P A H V L V R P
TGGTAATGAACACGGGCTCCGATTCTGAATATCCTTCTGTG (SEQ ID NO:71)
W * (SEQ ID NO:72)

rMOR-1D

Exon 3a ↓ Exon 8
-----AACCCAGACCTAGACCCCTGTGGAAGAACGTGTCTTTGAAATCGCGTGCAGAATCCAA
N H Q T * (SEQ ID NO:73) ↓ Exon 9b
TGTGGAGCACTTCCATTGTGGAGCCGCATTAATCTATAACAATGAACATAAATAGGGCCAGTG
TCCTGGCTCCAGATGCCCTGCGCACGTGCTCGTGGCCCCCTGGTAATGAACACGGGCTCCGATTC
TGAATATCCCTTCTGTG (SEQ ID NO:74)

FIG. 5(2)

Exon 3a ↓ **Exon 5b**

-----AACCACGAGGAGCCCTCAGTCAGTAGAGACATGATGTGAATGAACCAACTGATTAAACAAG

N H Q E P Q S V E T * (SEQ ID NO:75)

GTTTCTGAAACACTGAAATACAAACACAAATGTAGAGGTTACTAGAGAAAATTTGTAGCCTGAAAATTCAGGAAACCAAAATGAGTGTGAGTGATACATTTAAGGCCCTCAGAGAGATTTTATTTCATGACTAACACACATGACCCAAAGCACCTAAACTGTGTGATTAGATTACAAGACAATTCTAGAGCCTGGGACTAAAGAAAATGTTAGCCCTCACACAGACAGGCCCTCACACTTCAGTAATGGAATGAGCAAAATTAGATTAGTGAGAAAGATGGAGGAAGACTCGAAAATATTTTCATATCTTCCGTGTGAACTCCACAAGAAAACCAATAGAATAAACCAACCTGCTGGACCCCTGGTGCTCTTACC (SEQ ID NO:76)

[illegible]

rMOR-1B2 (1628 bp)

GTTACAGCCTACCTAGTCCGCAGCAGGCCCTTCAGCACCATGGACAGCACCGGCCCAGGGAACACGAGCGACTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCCAGCACCTGGCTCCTGGCTCAACTTGTCCACGTTGATGGCAACCAATC
CGATCCATGCGGTCTGAACCGCACCGGCTTGGCGGAACGACAGCCTGTGCCCTCAGACCGGACGCCCTTCCATGGT
CACAGCCATTACCATCATGCCCCCTCTACTCTATCGTGTGTAGTGGCCTCTTCGGAAACTTCCTGGTCATGTATGTGA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGACGCCCTTAGCGACCAG
TACACTGCCCTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAAACCATCCTCTGCAAGATCGTATTCA
ATAGATTACTACAACATGTTACCCAGCATATTACCCCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACC
CAGTCAAAGCCCTGGATTTCGGTACCCCGGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCTCTCTTCTTGCCAT
CGGTCTGCCCTGTAATGTTCATGGCAACCACAAATACAGGCAGGGTCCATAGATTGCACCCCTCACGTTCTCTCCACCCA
ACCTGCTACTGGGAGAACCTGCTCAAAATCTGTGCTTTATCTTCGCTTTCATCATGCCGGTCTCTCATCATCTGTGTG
TTACGGCCTGATGATCTTACGACTCAAGAGCGTTCGCATGCTATCGGGCTCCAAGAAAGACAGGAATTTGCGCAG
GATCACCCGGATGGTGGTGGTGGTGTATTATCGTCTGCTGGACCCCATCCACATCTACGTCAATCATCAATAA
GCGCTGATCACGATTCCAGAAACCCACATTTTCAGACCGTTTCTGCAATTGCTTTGGGTTACACGAACAGCT
GCCTGAATCCAGTTCTTTACGCCCTTCTGGGATGAATACTTCAAGCGATGCTTCAGAAAGATTCTGCATCCCAACCTC
GTCCACGATCGAACACAGCAAACTCCACTCGAGTCCGTCAAGACACTAGGGAACATCCCTCCACGGCTAATACAGTGA
TCGAACTAACCAAGGAGCCTCAGTCAGTAGAGACATGATGTGAATGAACCAACTGATTAAACAAGGTTTCTGAAC
ACTGAATAACACACAAATGTAGAGTTACTAGAGAAATTTGTAGCCTGAAAAATTCAATTACGGAAACCAAAATGAGT
GTGAGTGTATACATTTTAAGGCCTCAGAGAGATTTTATTTTCATGACTAACAAATGACCCAAAGCACCTAAACTGTGT
GATTAGATTACAAAGACAAATTCTAGAGCCTGGGACTAAAGAAATGTTAGCCCTCACACAGACAGCCTCACACTTCAG
TAATGGAAATGAGCAAAATTAGATTAGTGAGAAAGATGGAGGAAGACTCGAAATATTTTCATATCTTCTCTGTGGAACTC
CACAAAGAAACCAATAGAAATAAACCAACCTGCTGGACCCCTTGCTGCTTACC (SEQ ID NO:79)

rMOR-1B2 (394 aa)

MDSSTGPGNTSDCDPLAQASCPAPGSWLNLSHVVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYNNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRRTRMVLVVVAVFIVCWTPIHYYVIAKALITIPETTFQTVSWHFCIALGYTNSCLNPVL
LRLPGMKTSSDASEEFCIPTSSSTIEQQNSTRVRQNTREHPSTANTVDRTNHHQEPQSVET (SEQ ID NO:80)

FIG. 6A

rMOR-1C1 (1433 bp)

GTTACAGCCTACCTAGTCCGAGCAGGCCCTTCAGCACCATGGACAGCACCGGCCCAAGGGAACACACGACTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCAAGCACCTGGCTCCTGGCTCAACTTGTTCCCACTGTTGATGGCAACCAAGTC
CGATCCATGCGGTCTGAACCGCACCGGCTTGGCGGAACGACAGCCTGTGCCCTCAGACCGGCAAGCCCTTCCATGGT
CACAGCCATTACCATCATGGCCCTCTACTCTATCGTGTGTAGTGGCCCTCTTCGGAAACTTCCTGGTCAATGTATGTGA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGACGCCTTAGCGACCAG
TACACTGCCCTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAAACCATCCTCTGCAAGATCGTGATCTCA
ATAGATTACTACAACATGTTACACGACATATTCAACCCTCTGCACCATGAGCGTGACCGCTACATTGCTGTCTGCCACC
CAGTCAAAGCCCTGGATTTCGTAACCCCGGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCTCTCTTCTGCCAT
CGGTCTGCCCTGTAATGTTCATGGCAACCAACAATACAGGCAGGGGTCCATAGATTGCAACCCTCACGTTCTCCCAACCA
ACCTGGTACTGGGAGAACCTGCTCAAAATCTGTGTCTTTATCTTCGCTTTTCATCATGCGGTCCTCATCATCTGTGTG
TTACGGCCTGATGATCTTACGACTCAAGAGCGTTTCGCATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGCGCAG
GATCACCCGGATGGTGTGCTGGTGTGATTTATCGTCTGTGGACCCCAATCCACATCTACGTCAATCATCAAA
GCGTGATCACGATTCCAGAAACCAACATTTACAGACCGTTTCTGGCACTTCTGCAATTGGTTACACGAACAGCT
GCCTGAATCCAGTTCTTACGCCCTTCTTGATGAATAACTTCAAGCGATGCTTCAGAGAGTTCTGCAATCCCAACCTCGTCC
ACGATCGAACAGCAAAACTCCACTCGAGTCCGTCAGAAACACTAGGGAACATCCCTCCACGGCTAATACAGTGATCGA
ACTAACCAAGAGTTACAGGACAGACCTAGACCTGTGGAAAGACGTGCTTTGAAATCGCGTGCAAGATCCAATGTGG
AGCACTTCCATTGTGGAGCCGCAATTAATCTATAACAATGTGAATTTTCATCTAAACACAGGATGTGCTAGTGAGAAATT
TGGAGGTGCAGGC (SEQ ID NO:81)

rMOR-1C1 (451 aa)

MDSSTGPGNTSDCDPLAQASCPAPGSWLNLSHV DGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLLVVAVFIVCWTPIHIVIIKALITPETTFQTVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCFREFCIPTSSSTIEQQNSTRVRQNTREHPSTANTVDRTNHQPALAVSVAQIFTGYPSPTHGEKPKCSYRDRPRP
CGRTWSLKSRAESNVEHFHCGAALIYNNVNF I (SEQ ID NO:82)

FIG. 6B

rMOR-1C2 (1480 bp)

GTTACAGCCTACCTAGTCCGCAGCAGGCCTTCAGCACCATGGACAGCAGCACCGGCCACGGGAACACGAGCTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCCAGCACCTGGCTCCTGGCTCAACTGTGCCACGTTGATGGCAACCAAGTC
CGATCCATGCGGTCTGAACCGCACCGGCTTGGCGGGAACGACAGCCTGTGCCCTCAGACCGGACGCCCTTCCATGGT
CACAGCCATTACCATCATGGCCCTCTACTCTATCGTGTGTAGTGGCCCTCTTCGGAAACTTCCTGGTCAATGTATGTGA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGACGCCCTTAGCGACCAG
TACACTGCCCTTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAAACCATCCTCTGCAAGATCGTGATCTCA
ATAGATTACTAACACATGTTACACAGCATATTACCCCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACC
CAGTCAAAGCCCTGGATTTCCGTACCCCCCGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCTCTCTTCTGCCAT
CGGTCTGCCGTGAATGTTTCATGGCAACCAACAATAACAGCAGGGGTCCATAGATTGCACCCCTACGTTCTCCACCCCA
ACCTGGTACTGGGAGAACCTGCTCAAAATCTGTGTCTTTATCTTCGCTTTTCATCATGCCGTCCTCATCATCACTGTGTG
TTACGGCCTGATGATCTTACGACTCAAGAGCGTTTCGCATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGCGCAG
GATCACCCGGATGGTGGTGGTGGTGTATTATCGTCTGCTGGACCCCATCCACATCTACGTCAATCATCAAA
GCGTGATCACGATTCCAGAAACCAACATTTTCAGACCGTTTCTCGCACTTCTGCAATTGGTTTACACGAACAGCT
GCCGTGAATCCAGTTCTTACGCCCTTCTCGATGAATACTCAAGCGATGCTTCAGAGAGTTCTGCATCCCAACCTCGTCC
ACGATCGAACAGCAAAACTCCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGGATCGA
ACTAACCAACAGCCAGCCCTGGCAGTCAGCGTGGCCAGATCTTTACAGGATATCCTTCTCCGACTCATGGTGAAAAAC
CCTGCAAGAGTTACAGGGACAGACCTAGACCCCTGTGGAAAGAACGTGGTCTTTGAAATCGCGTGCAGAAATCCAATGTGG
AGCACTTCCATTGTGGAGCCGCAATTAATCTATAACAATGAACATAAGGGCCAGTGTCTGGCTCCAGATGCCTGC
GCACGTGCTCGTGCGCCCTGGTAATGAACACGGGCTCCGATTCTGAATATCCTTCTGTG (SEQ ID NO:83)

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rMOR-1C2 (468 aa)

MDSSTGPGNTSDCSDPLAQASCPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNMFSTIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRITRMVLVVAVFIVCWTPHIYVIAKALITIPETTFQTVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCFREFCIPTSSTIEQQNSTVRQNTREHPSTANTVDRTNHQPALAVSVAQIFTGYPSPTHGEKPKCKSYRDRPRP
CGRTWSLKSRAESNVEHFHCGAALIYNNELKIGPVSWLQMPAHVLVRPW (SEQ ID NO:84)

FIG. 6C

rMOR-1D (1385 bp)

GCCTACCTAGTCCGCAGCAGGCCTTCAGCACCATGGACAGCAGCACCGGCCAGGGAACACGAGCTGCTCAGACC
CCTTAGCTCAGGCAAGTTGCTCCCCAGCACCTGGCTCCTGGCTCAACTTGTCACAGTTGATGGCAACCAAGTCCGATCC
ATGCGGTCTGAACCGCACCGGCTTGGCGGGAACGACAGCCTGTGCCCTCAGACCGCAGCCCTTCCATGGTCAACAGC
CATTACCATCATGGCCCTCTACTCTATCGTGTGTAGTGGGCCCTCTTCGGAAACTTCCTGGTCAATGTATGTGATTGTAA
GATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGACGCCCTTAGCGACCAGTACACT
GCCCTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAACCATCCTCTGCAAGATCGTGATCTCAATAGAT
TACTACAAACATGTTCAACAGCATATTACCCCTCTGCACCATGAGCGTGGACCGCTACATTGCTGTCTGCCACCCAGTCA
AAGCCCTGGATTTCCGTACCCCCGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCTCTCTTCTGCCATCGGTCT
GCCTGTAAATGTTTCATGGCAACCAACAAATACAGGCAGGGTCCATAGATTGCACCCCTCACGTTCTCCACCCCAACCTGG
TACTGGGAGAACCTGCTCAAAATCTGTGTCTTTGCTTCGCTTTCATCATGCGGTCCTCATCATCTGTGTGTACCG
CCTGATGATCTTACGACTTAAGAGCGTTTCGCAATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGCGCAGGATCAC
CCGGATGGTGTGGTGTGGCTGTATTATCGTCTGTGCTGGACCCCATCCACATCTACGTCAATCAACAAAGCGCTG
ATCACGATTCCAGAAACCAACATTTTCAGACCGTTTCCCTGGCACTTCTGCAATTGGGTTACACGAACAGCTGCCCTGA
ATCCAGTTCTTTACGCCTTCCTGGATGAACACTTCAAGCGATGCTTCAGAGAGTTCTGCATCCCAACCTCGTCCACGATC
GAACAGCAAAACTCCACTCGAGTCCGTGAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGGATCGAACTAAC
CACCAGACCTAGACCCCTGTGGAAGAACGTGGTCTTTGAAATCGCGTGCAGAAATCCAATGTGGAGCACTTCCATTGTGGA
GCCGCATTAACTATAACAATGAACATAAGGGCCAGTGTCTGCTCCAGATGCCTGCGCACGTGCTCGTGTGCGGCC
CCTGGTAATGAACACGGGCTCCGATTCTGAATATCCTTCTGTG (SEQ ID NO:85)

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rMOR-1D (387 aa)

MDSSTGPGNTSDCSDPLAQASCPAPGSWLNLSHVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMAATTKYRQGSIDCTLTFSHPTWYWENLLKICVFVFAFIMPVLHITV
CYGLMILRLKSVRMLSGSKEKDRNLRRITRMVLVVVAVFIVCWTPIHIVYVIAKALITIPETTFQTVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCREFCIPTSSTIEQQNSTVRQNTREHPSTANTVDRTNHQ (SEQ ID NO:86)

FIG. 6D

rMOR-1E (2078 bp)

GTACAGCCTACCTAGTCCGCAGCAGGCCTTCAGCACCATGGACAGCACCGGCCAGGGAACACAGCGACTGCT
CAGACCCCTTAGCTCAGGCAAGTTGCTCCCCAGCACCTGGCTCCTGGCTCAACTTGTCCCACGTTGATGGCAACCAATC
CGATCCATGCGGTCTGAACCGCACCGGGCTTGGCGGGAACGACAGCCTGTGCCCTCAGACCGGACGCCCTTCCATGGT
CACAGCCATTACCATCATGGCCCTCTACTCTATCGTGTGTAGTGGGCCCTCTTCGGAAACTTCCTGGTCAATGTAATGTA
TTGTAAGATACACCAAAATGAAGACTGCCACCAACATCTACATTTTCAACCTTGCTCTGGCAGACGCCCTTAGCGACCAG
TACACTGCCCTTTTCAGAGTGTCAACTACCTGATGGGAACATGGCCCTTCGGAAACCATCCTCTGCAAGATCGTGATCTCA
ATAGATTACTACAACATGTTCAACCAGCATATTCAACCCTCTGCACCATGAGCGTGGACCGCTACATTTGCTGTCTGCCACC
CAGTCAAAGCCCTGGATTTCCGTACCCCCGAAATGCCAAATCGTCAACGTCTGCAACTGGATCCTCTCTTCTGCCAT
CGGTCTGCCGTAAATGTTTCATGGCAACCACAAATACAGGACGGGTCCATAGATTGCACCCCTCACGTTCTCTCCACCCA
ACCTGGTACTGGGAGAACCTGCTCAAAATCTGTGCTTTATCTTCGCTTTTCATCATGCCGGTCTCTCATCATCTGTGTG
TTACGGCCTGATGATCTTACGACTCAAGAGCGTTTCGCATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGCGCGG
GATCACCCGGATGGTGTGCTGCTGGCTGATTTATCGTCTGTGACCCCATCCACATCTACGTCAATCATCAAA
GCGTGATCACGATTCCAGAAACCAATTTTCAGACCGTTTCTGGCACTTCTGCAATGCTTTGGTTACACGAACAGCT
GCCTGATCCAGTTCTTTACGCCCTTCTGATGAATACTCAAGCGATGCTTCAGAGAGTTCTGCAATCCCACCTCGTCC
ACGATCGAACAGCAAACTCCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCCACGGCTAATACAGTGGATCGA
ACTAACCAACGAGGAGCAGATTATGAGGATTAAATACA^{25/26}AAAGACTACCACGTCTTCAGAGGAGCAGCCAGAGGGA
GGCCCTTGCCCCCAATGTTAGGTGCTCCCACCTTGTCTCTCCCATCACACATCTCTCACTGTTCCCTTTTGTTC
GCTATGGCTACCCGGCATAGCCTTTATTCAGTCTTTCTGACTGACCTCAGATTTATGCAATACAACTAGATGGATCCGC
CTCAGGAGACAGGAATGCTCATACCGAAGTGGGAAGTGGCTAATGCAATACACGTGAGCCAACACCCCAAGAGAG
CATGGTGGTAATGGCGGCAGAGTCATCCCCACTCAAAGGCAATTATTAAACAATTTATCTCCCTGCTTCCAGCTCAGA
AATCAGAGCCAGACAGAAATGGGTTCCTGTGCT
CATTGTTATCCACATCAACACATAACCCCTTTACTTTTCTAAGCAGCCCTCTTTTAGGGGTTTTCAAACTCTCGCCTGC
ACTTTGAAAGGGTAAGGATTTAAATTGATTTTCT
TGAAACTATCTATACAAACTGAGCTTCAAATCTTTGGCATTTAAATATTTTGTCTTTCATTGGAGAAAGGAAGAGCATA
GGAAAGCTTGGGCTCTTCCTCCCCTCCCTAGGTGTCT
GTAGCTTCTCTAGGACACTGTGGGCCCTTCTTATCCTGCCTGACCCACCTGACCTTCTCTAATGGTCAACCTCTCTATT
CCAGCACATTCTCTGTTTC (SEQ ID NO:87)

FIG. 6E(1)

rMOR-1E (390 aa)

MDSSSTGPGNTSDCSDPLAQASCSPAGSWLNLSHVDGNQSDPCGLNRTGLGGNDSLCPQTGSPSMVTAITIMALYSIVCVVG
LFGNFLVMYVIVRYTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPFGTILCKIVISIDYYNNMFTSIFTLCTMSVDRY
IAVCHPVKALDFRTPRNAKIVNVCNWILSSAIGLPVMFMATTKYRQGSIDCTLTFSHPTWYWENLLKICVFIFAFIMPVLIITV
CYGLMILRLKSVRMLSGSKEKDRNLRGITRMVLVVVAVFIVCWTPIHIVYVIAKALITIPETTFQTVSWHFCIALGYTNSCLNPVL
YAFLDENFKRCFREFCIPTSSTIEQQNSTRVRQNTREHPSTANTVDRTNHQGAEL (SEQ ID NO:88)

FIG. 6E(2)